

1 / 4 9

SEQUENCE LISTING

<110> National Agricultural Research Organization

<120> JUVENILE HORMONE TRANSMETHYLASE GENES

AND METHOD OF USING THE SAME

<130> ARO-A0301P

<160> 36

<170> PatentIn version 3.1

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<211> 2890

<212> DNA

<213> Bombyx mori

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<221> CDS

<222> (125)..(961)

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Met Asn Asn Ala Asp Leu Tyr Arg Lys Ser Asn Ser Leu Gln Lys								
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Arg Asp Ala Leu Arg Cys Leu Glu Glu His Ala Asn Lys Ile Lys Trp								
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aaa aaa atc	ggt gat	aga gtc	ata gat	ttg ggt	tgc gct	gac ggt	agt	265
Lys Lys Ile Gly Asp Arg Val Ile Asp Leu Gly Cys Ala Asp Gly Ser								
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gtt act	gat att	ttg aaa	gtt tac	atg cca	aaa aat	tac gga	aga tta	313
Val Thr Asp Ile Leu Lys Val Tyr Met Pro Lys Asn Tyr Gly Arg Leu								
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Val Gly Cys Asp Ile Ser Glu Glu Met Val Lys Tyr Ala Asn Lys His								
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cac ggc	ttc ggt	agg act	tcg ttc	agg gtg	ctc gac	ata gag	ggc gat	409
His Gly Phe Gly Arg Thr Ser Phe Arg Val Leu Asp Ile Glu Gly Asp								
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Thr Leu His Trp Ile Arg Asp Gln Glu Arg Ala Phe Arg Asn Ile Phe			
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Asn Leu Leu Gly Asp Glu Gly Asp Cys Leu Leu Phe Leu Gly His			
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His Ser Trp Leu Glu His Val Asp Arg Phe Ile Ser Pro Tyr His Asp			
160	165	170	175
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Asn Glu Asp Pro Glu Lys Glu Val Lys Lys Ile Met Glu Arg Val Gly			
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210 215 220

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Ile Pro Lys Asp Ile Leu Glu Asp Phe Leu Glu Asp Tyr Ile Asp Val

225 230 235

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Ser Val Ser Ile Lys Phe Asn Tyr Lys Val Ile Ser Val Tyr Ala Arg
260 265 270

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Lys Leu Cys Leu Ser Leu Met

275

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7 / 4 9

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35 40 45

Thr Asp Ile Leu Lys Val Tyr Met Pro Lys Asn Tyr Gly Arg Leu Val

50 55 60

Gly Cys Asp Ile Ser Glu Glu Met Val Lys Tyr Ala Asn Lys His His
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Gly Phe Gly Arg Thr Ser Phe Arg Val Leu Asp Ile Glu Gly Asp Leu
85 90 95

Thr Ala Asp Leu Lys Gln Gly Phe Asp His Val Phe Ser Phe Tyr Thr
100 105 110

Leu His Trp Ile Arg Asp Gln Glu Arg Ala Phe Arg Asn Ile Phe Asn
115 120 125

Leu Leu Gly Asp Glu Gly Asp Cys Leu Leu Leu Phe Leu Gly His Thr
130 135 140

Pro Ile Phe Asp Val Tyr Arg Thr Leu Ser His Thr Glu Lys Trp His
145 150 155 160

Ser Trp Leu Glu His Val Asp Arg Phe Ile Ser Pro Tyr His Asp Asn
165 170 175

Glu Asp Pro Glu Lys Glu Val Lys Lys Ile Met Glu Arg Val Gly Phe
180 185 190

Ser Asn Ile Glu Val Gln Cys Lys Thr Leu Phe Tyr Val Tyr Asp Asp

195 200 205

Leu Asp Val Leu Lys Lys Ser Val Ala Ala Ile Asn Pro Phe Asn Ile

210 215 220

Pro Lys Asp Ile Leu Glu Asp Phe Leu Glu Asp Tyr Ile Asp Val Val

225 230 235 240

Arg Glu Met Arg Leu Leu Asp Arg Cys Asn Asn Asn Val Gly Glu Ser

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<222> (1)..(894)

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Val Leu Met Asp Phe Val Lys Pro Leu Leu Pro Ile Arg Gly Gln Leu
50 55 60

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Val Gly Thr Asp Ile Ser Ser Gln Met Val His Tyr Ala Ser Lys His
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Tyr Gln Arg Glu Glu Arg Thr Arg Phe Gln Val Leu Asp Ile Gly Cys
85 90 95

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Phe Tyr Cys Leu His Trp	Val Gln Asn Leu Lys Gly	Ala Leu Gly Asn	
115	120	125	
atc tac aat ctt ctg aag	ccc gaa ggt ggc gac	tgc ctc ctg gca ttt	432
Ile Tyr Asn Leu Leu Lys Pro Glu	Gly Gly Asp Cys Leu	Leu Ala Phe	
130	135	140	
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Asp Lys Trp Ser Thr Tyr Met	Gln Asp Val Glu Asn Phe	Ile Ser Pro	
165	170	175	
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Leu His Tyr Ser Leu Asn Pro	Gly Glu Glu Phe Ser	Gln Leu Leu Asn	
180	185	190	
gat gtg ggt ttc	gtg caa cac aat	gtg gaa att cga aac gaa	624

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195 200 205

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210 215 220

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Pro Phe Leu Glu Arg Met Pro Ala Asp Leu His Glu Gln Phe Leu Asp
225 230 235 240

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245 250 255

aat gag gat caa aag ttc cta tct ccc tat aaa ctg gtg gtg gcc tat 816
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260 265 270

gct cgc aag act cct gaa ttt gtg aat aat gtt ttc ctg gag cct aca 864
Ala Arg Lys Thr Pro Glu Phe Val Asn Asn Val Phe Leu Glu Pro Thr
275 280 285

cat caa aac ttg gtt aag gga ata aat taa ttttatttta caaattaaca 914
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Ser Asp Gly Glu Asp Ala Leu Leu Asp Val Gly Ser Gly Ser Gly Asn

35 40 45

Val Leu Met Asp Phe Val Lys Pro Leu Leu Pro Ile Arg Gly Gln Leu

50 55 60

Val Gly Thr Asp Ile Ser Ser Gln Met Val His Tyr Ala Ser Lys His

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Tyr Gln Arg Glu Glu Arg Thr Arg Phe Gln Val Leu Asp Ile Gly Cys

1 4 / 4 9

85 90 95

Glu Arg Leu Pro Glu Glu Leu Ser Gly Arg Phe Asp His Val Thr Ser

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Phe Tyr Cys Leu His Trp Val Gln Asn Leu Lys Gly Ala Leu Gly Asn

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Ile Tyr Asn Leu Leu Lys Pro Glu Gly Gly Asp Cys Leu Leu Ala Phe

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Leu Ala Ser Asn Pro Val Tyr Glu Val Tyr Lys Ile Leu Lys Thr Asn

145 150 155 160

Asp Lys Trp Ser Thr Tyr Met Gln Asp Val Glu Asn Phe Ile Ser Pro

165 170 175

Leu His Tyr Ser Leu Asn Pro Gly Glu Glu Phe Ser Gln Leu Leu Asn

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Asp Val Gly Phe Val Gln His Asn Val Glu Ile Arg Asn Glu Val Phe

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Val Tyr Glu Gly Val Arg Thr Leu Lys Asp Asn Val Lys Ala Ile Cys

210 215 220

1 5 / 4 9

Pro Phe Leu Glu Arg Met Pro Ala Asp Leu His Glu Gln Phe Leu Asp

225 230 235 240

Asp Phe Ile Asp Ile Val Ile Ser Met Asn Leu Gln Gln Gly Glu Asn

245 250 255

Asn Glu Asp Gln Lys Phe Leu Ser Pro Tyr Lys Leu Val Val Ala Tyr

260 265 270

Ala Arg Lys Thr Pro Glu Phe Val Asn Asn Val Phe Leu Glu Pro Thr

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Arg Asp Gly Glu Glu Val Ala Leu Leu Asp Ile Gly Cys Gly Ser Gly

35 40 45

gac gtg ttg gtg gac tac att cta ccg gtg ctg agc cgc gga agc act 192

Asp Val Leu Val Asp Tyr Ile Leu Pro Val Leu Ser Arg Gly Ser Thr

50 55 60

cct gtg gcg cgc gca ttg gcg aca gac atc tcg gag cag atg gtg cgc 240

Pro Val Ala Arg Ala Leu Ala Thr Asp Ile Ser Glu Gln Met Val Arg

65 70 75 80

cat gca cgt gaa tcg tac cgt cac gtt aag acg atc gag ttc gac acc 288

His Ala Arg Glu Ser Tyr Arg His Val Lys Thr Ile Glu Phe Asp Thr

85 90 95

ctt gac atc ggc atc aaa ctc gat agt gca aag ttg tcc cgc tgg gga 336

1 7 / 4 9

Leu Asp Ile Gly Ile Lys Leu Asp Ser Ala Lys Leu Ser Arg Trp Gly

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Gln Phe Ser His Val Thr Ser Phe Tyr Cys Leu His Trp Val Gln Asn

115 120 125

cag cac gta gcc ttt tcc aac atc tac aac ctt ctg cag cat ggc ggt 432

Gln His Val Ala Phe Ser Asn Ile Tyr Asn Leu Leu Gln His Gly Gly

130 135 140

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Asp Cys Leu Leu Val Phe Leu Ala Asn Asn Pro Ile Phe Asp Ile Tyr

145 150 155 160

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165 170 175

gaa aag tac att tcg ccc tac cag tat tgt gaa aat cca gca agt gag 576

Glu Lys Tyr Ile Ser Pro Tyr Gln Tyr Cys Glu Asn Pro Ala Ser Glu

180 185 190

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Ile Glu Asp Leu Leu Cys Thr Val Gly Phe Gln Gln Tyr Gln Ile Gln

195 200 205

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225	230	235
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Gln Asp Arg Phe Leu Leu Asp Tyr Ile Ala Val Val Arg Gln Met Tyr		
245	250	255
ttg acc aaa act ggc agc gaa gag aat gat tgc aat ctt caa ttc ata	816	
Leu Thr Lys Thr Gly Ser Glu Glu Asn Asp Cys Asn Leu Gln Phe Ile		
260	265	270
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<213> Anopheles gambiae

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25

30

Arg Asp Gly Glu Glu Val Ala Leu Leu Asp Ile Gly Cys Gly Ser Gly

35

40

45

Asp Val Leu Val Asp Tyr Ile Leu Pro Val Leu Ser Arg Gly Ser Thr

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Pro Val Ala Arg Ala Leu Ala Thr Asp Ile Ser Glu Gln Met Val Arg

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His Ala Arg Glu Ser Tyr Arg His Val Lys Thr Ile Glu Phe Asp Thr

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90

95

Leu Asp Ile Gly Ile Lys Leu Asp Ser Ala Lys Leu Ser Arg Trp Gly

100

105

110

Gln Phe Ser His Val Thr Ser Phe Tyr Cys Leu His Trp Val Gln Asn

115

120

125

2 0 / 4 9

Gln His Val Ala Phe Ser Asn Ile Tyr Asn Leu Leu Gln His Gly Gly

130 135 140

Asp Cys Leu Leu Val Phe Leu Ala Asn Asn Pro Ile Phe Asp Ile Tyr

145 150 155 160

Asn Gln Leu Ser Arg Ser Pro Lys Trp Ser Lys Tyr Met Tyr Asp Val

165 170 175

Glu Lys Tyr Ile Ser Pro Tyr Gln Tyr Cys Glu Asn Pro Ala Ser Glu

180 185 190

Ile Glu Asp Leu Leu Cys Thr Val Gly Phe Gln Gln Tyr Gln Ile Gln

195 200 205

Val Arg Asp Lys Leu Tyr Val Tyr Glu Gly Leu Asp Asn Leu Lys Arg

210 215 220

Ala Val Leu Ala Val Asn Pro Phe Ser Glu Arg Met Pro Pro Glu Leu

225 230 235 240

Gln Asp Arg Phe Leu Leu Asp Tyr Ile Ala Val Val Arg Gln Met Tyr

245 250 255

Leu Thr Lys Thr Gly Ser Glu Glu Asn Asp Cys Asn Leu Gln Phe Ile

260 265 270

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Met Asn

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Asn Ala Val Leu Tyr Glu Gln Ala Asn Ser Met Gln Lys Arg Asp Ala

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10

15

22 / 49

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Ile Ser Asn Ile Leu Asp Val Gly Cys Gly Asp Gly Cys Val Thr Ser			
35	40	45	50
atg ctt aaa aag tac atc cct act gac ttc aag ctg ctc ggc tgt gac			308
Met Leu Lys Lys Tyr Ile Pro Thr Asp Phe Lys Leu Leu Gly Cys Asp			
55	60	65	
atc agt gag aag atg gtg aat ttc gcc aat gac cac cat tgc aat gaa			356
Ile Ser Glu Lys Met Val Asn Phe Ala Asn Asp His His Cys Asn Glu			
70	75	80	
cag acg tcg ttc aca gtg ctg gac atc gca gga gat ata ccc gaa ggt			404
Gln Thr Ser Phe Thr Val Leu Asp Ile Ala Gly Asp Ile Pro Glu Gly			
85	90	95	
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Met Lys Gly Lys Phe Asp His Val Phe Ser Phe Tyr Ala Leu His Trp			
100	105	110	
gtc ttg gat caa gag cgc gta ttc agg aat att tac gat ttg ctg agt			500
Val Leu Asp Gln Glu Arg Val Phe Arg Asn Ile Tyr Asp Leu Leu Ser			

2 3 / 4 9

115

120

125

130

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 Lys Asp Gly Glu Cys Phe Thr Ile Phe Val Ala Gly Ala Pro Val Phe

135

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145

gac ttg tac cgc att tta tcg cgt aac aac aaa tgg agc act ctg ctt 596
 Asp Leu Tyr Arg Ile Leu Ser Arg Asn Asn Lys Trp Ser Thr Leu Leu

150

155

160

aaa gat gtc gag aaa tac ata tcg cca tac cac gac tca cag gat cca 644
 Lys Asp Val Glu Lys Tyr Ile Ser Pro Tyr His Asp Ser Gln Asp Pro

165

170

175

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185

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225

24 / 49

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230 235 240

aaa att gtg tct aag tat aat acc gat gag gca agt gtg aac ttc aaa 884
Lys Ile Val Ser Lys Tyr Asn Thr Asp Glu Ala Ser Val Asn Phe Lys
245 250 255

245 250 255

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<211> 273

<212> PRT

<213> Spodoptera litura

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Lys Ser Ile Ser Asn Ile Leu Asp Val Gly Cys Gly Asp Gly Cys Val

35 40 45

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50 55 60

Cys Asp Ile Ser Glu Lys Met Val Asn Phe Ala Asn Asp His His Cys

65 70 75 80

Asn Glu Gln Thr Ser Phe Thr Val Leu Asp Ile Ala Gly Asp Ile Pro

85 90 95

Glu Gly Met Lys Gly Lys Phe Asp His Val Phe Ser Phe Tyr Ala Leu

100 105 110

His Trp Val Leu Asp Gln Glu Arg Val Phe Arg Asn Ile Tyr Asp Leu

115 120 125

Leu Ser Lys Asp Gly Glu Cys Phe Thr Ile Phe Val Ala Gly Ala Pro

130 135 140

Val Phe Asp Leu Tyr Arg Ile Leu Ser Arg Asn Asn Lys Trp Ser Thr

145 150 155 160

Leu Leu Lys Asp Val Glu Lys Tyr Ile Ser Pro Tyr His Asp Ser Gln
165 170 175

Asp Pro Ala Lys Glu Met Arg Lys Val Leu Glu Lys Val Gly Tyr Val
180 185 190

Asp Tyr Lys Val Glu Cys Lys Asn Leu Val Tyr Met Tyr Asn Asn Phe
195 200 205

Ala Ser Leu Trp Lys Thr Leu Gln Ala Ile Asn Pro Phe Asn Ile Pro
210 215 220

Lys Asp Met Glu Glu Asp Phe Lys Gln Asp Tyr Leu Asn Ile Leu Lys
225 230 235 240

Asp Met Lys Ile Val Ser Lys Tyr Asn Thr Asp Glu Ala Ser Val Asn
245 250 255

Phe Lys Tyr Arg Leu Leu Val Val His Ala Arg Lys Pro Ala Ser Glu
260 265 270

Phe

27 / 49

<211> 1193

<212> DNA

<213> *Helicoverpa armigera*

<220>

<221> CDS

<222> (124)..(978)

<223>

<400> 9

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aagaatcata aactaaacaa atcaatatca ccaaattcaa atacctataa aaaaatcctt 120

aaa atg aat aac gcg gtc ttg tat gaa aaa agc aat agc ttg cag aag 168

Met Asn Asn Ala Val Leu Tyr Glu Lys Ser Asn Ser Leu Gln Lys

1 5 10 15

aga gat gct atc atg tgt cta gaa gaa tac gct tcg aaa att aag tgg 216

Arg Asp Ala Ile Met Cys Leu Glu Glu Tyr Ala Ser Lys Ile Lys Trp

20 25 30

aag aag agt aat aat aat att ctt gac ata ggc tgt ggg gat gga agc 264

Lys Lys Ser Asn Asn Asn Ile Leu Asp Ile Gly Cys Gly Asp Gly Ser

35 40 45

28 / 49

gtg act aat atg ctg aag aaa tac atc cct act gag tac aag ttg ctt			312
Val Thr Asn Met Leu Lys Lys Tyr Ile Pro Thr Glu Tyr Lys Leu			
50	55	60	
ggc tgt gat att agc gag aag atg gtg aac ttc gcg aat gat cat cat			360
Gly Cys Asp Ile Ser Glu Lys Met Val Asn Phe Ala Asn Asp His His			
65	70	75	
tgt aac gaa cag act tct ttc acc gtg ctc gat att gag gga gac cta			408
Cys Asn Glu Gln Thr Ser Phe Thr Val Leu Asp Ile Glu Gly Asp Leu			
80	85	90	95
cct gaa ggt atg aag gga aac ttc gac cac gtt ttc tcg ttc tac gct			456
Pro Glu Gly Met Lys Gly Asn Phe Asp His Val Phe Ser Phe Tyr Ala			
100	105	110	
ctg cac tgg gtt aat aac caa gaa cga gca ttc aaa aac ata tac aac			504
Leu His Trp Val Asn Asn Gln Glu Arg Ala Phe Lys Asn Ile Tyr Asn			
115	120	125	
ctt cta agc gag gat ggg gag tgc ttc acg ata ttc gta gcc tgg gct			552
Leu Leu Ser Glu Asp Gly Glu Cys Phe Thr Ile Phe Val Ala Trp Ala			
130	135	140	
cct gtg ttt gac gtg tac cga gtg ctc gcg cgc aac aac aag tgg agt			600
Pro Val Phe Asp Val Tyr Arg Val Leu Ala Arg Asn Asn Lys Trp Ser			

29 / 49

145	150	155	
<pre> caa tgg gtg cat gat gtc gac aga tac ata tcg ccc tac cac gac tct Gln Trp Val His Asp Val Asp Arg Tyr Ile Ser Pro Tyr His Asp Ser </pre>			
160	165	170	175
<pre> ttg gag ccg gaa aaa gat tta aag gct atg ata gac aaa att gga ttc Leu Glu Pro Glu Lys Asp Leu Lys Ala Met Ile Asp Lys Ile Gly Phe </pre>			
180	185	190	
<pre> gtt gac atc gat gtg gaa tgt aaa gaa ttg gta ttc gtg tac gac aac Val Asp Ile Asp Val Glu Cys Lys Glu Leu Val Phe Val Tyr Asp Asn </pre>			
195	200	205	
<pre> ata cat att ttg cga aaa gcg tta aca gca atc aac cct ttc aaa atc Ile His Ile Leu Arg Lys Ala Leu Thr Ala Ile Asn Pro Phe Lys Ile </pre>			
210	215	220	
<pre> ccc aag gaa aaa tat gat gat ttc atg gaa gac tat atg gat ata ctg Pro Lys Glu Lys Tyr Asp Asp Phe Met Glu Asp Tyr Met Asp Ile Leu </pre>			
225	230	235	
<pre> aaa gaa cta caa att tta gac aag tac aac aat aat tat gaa aag agc Lys Glu Leu Gln Ile Leu Asp Lys Tyr Asn Asn Asn Tyr Glu Lys Ser </pre>			
240	245	250	255

30 / 49

gtt gaa ttc aat tac cgt ttg ctt gta gtg tat gcc cga aaa cct gac 936
 Val Glu Phe Asn Tyr Arg Leu Leu Val Val Tyr Ala Arg Lys Pro Asp

260 265 270

tcg cag gat aaa atg tta gaa gct cta aat gga caa acg tag 978
 Ser Gln Asp Lys Met Leu Glu Ala Leu Asn Gly Gln Thr
 275 280

actgaaaaac ttatattttt agttacggca aaatacagtg tagaacagtt atttgttagtt 1038

aaggatgaat gtatagtgtt tctcttcagg ttttagtttg ggcctggtat gaaatgttgt 1098

tttttaagt aagctatttt ggtaatgtaa actatttta aaggcaggaa aataatctgt 1158

gtgtgagcaa aaaaaaaaaa aaaaaaaaaa aaaaa 1193

<210> 10

<211> 284

<212> PRT

<213> Helicoverpa armigera

<400> 10

Met Asn Asn Ala Val Leu Tyr Glu Lys Ser Asn Ser Leu Gln Lys Arg

1 5 10 15

3 1 / 4 9

Asp Ala Ile Met Cys Leu Glu Glu Tyr Ala Ser Lys Ile Lys Trp Lys

20 25 30

Lys Ser Asn Asn Asn Ile Leu Asp Ile Gly Cys Gly Asp Gly Ser Val

35 40 45

Thr Asn Met Leu Lys Lys Tyr Ile Pro Thr Glu Tyr Lys Leu Leu Gly

50 55 60

Cys Asp Ile Ser Glu Lys Met Val Asn Phe Ala Asn Asp His His Cys

65 70 75 80

Asn Glu Gln Thr Ser Phe Thr Val Leu Asp Ile Glu Gly Asp Leu Pro

85 90 95

Glu Gly Met Lys Gly Asn Phe Asp His Val Phe Ser Phe Tyr Ala Leu

100 105 110

His Trp Val Asn Asn Gln Glu Arg Ala Phe Lys Asn Ile Tyr Asn Leu

115 120 125

Leu Ser Glu Asp Gly Glu Cys Phe Thr Ile Phe Val Ala Trp Ala Pro

130 135 140

Val Phe Asp Val Tyr Arg Val Leu Ala Arg Asn Asn Lys Trp Ser Gln

145 150 155 160

Trp Val His Asp Val Asp Arg Tyr Ile Ser Pro Tyr His Asp Ser Leu
165 170 175

Glu Pro Glu Lys Asp Leu Lys Ala Met Ile Asp Lys Ile Gly Phe Val
180 185 190

Asp Ile Asp Val Glu Cys Lys Glu Leu Val Phe Val Tyr Asp Asn Ile
195 200 205

His Ile Leu Arg Lys Ala Leu Thr Ala Ile Asn Pro Phe Lys Ile Pro
210 215 220

Lys Glu Lys Tyr Asp Asp Phe Met Glu Asp Tyr Met Asp Ile Leu Lys
225 230 235 240

Glu Leu Gln Ile Leu Asp Lys Tyr Asn Asn Asn Tyr Glu Lys Ser Val
245 250 255

Glu Phe Asn Tyr Arg Leu Leu Val Val Tyr Ala Arg Lys Pro Asp Ser
260 265 270

Gln Asp Lys Met Leu Glu Ala Leu Asn Gly Gln Thr
275 280

3 3 / 4 9

<210> 11

<211> 17

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 11

ttttttttt ttttg

17

<210> 12

<211> 10

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 12

gatcatagcc

10

<210> 13

<211> 25

3 4 / 4 9

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 13

aagccgcagt aagatggcgg tggtt

25

<210> 14

<211> 25

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 14

caacaccgcc atcttactgc ggctt

25

<210> 15

<211> 30

<212> DNA

<213> Artificial

3 5 / 4 9

<220>

<223> an artificially synthesized primer sequence

<400> 15

aaacatatac acaatgcaga tttataccgc

30

<210> 16

<211> 30

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 16

aaggatccaa tcacgaaaat ctgggaagac

30

<210> 17

<211> 30

<212> DNA

<213> Artificial

<220>

3 6 / 4 9

<223> an artificially synthesized primer sequence

<400> 17

aaacatatac atcaggcctc tctatatcag

30

<210> 18

<211> 34

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 18

aaggatccga ctctgttaac aaatgcaatt actg

34

<210> 19

<211> 23

<212> DNA

<213> Artificial

<220>

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3 7 / 4 9

<220>

<221> misc_feature

<222> (6)..(6)

<223> "n"=A, T, G or C

<220>

<221> misc_feature

<222> (15)..(15)

<223> "n"=A, T, G or C

<400> 19

atggtnaart aygcnaayaa rca

23

<210> 20

<211> 23

<212> DNA

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<220>

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<220>

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<222> (6)..(6)

<223> "n"=A, T, G or C

<220>

<221> misc_feature

<222> (12)..(12)

<223> "n"=A, T, G or C

<400> 20

taraangara anacrtgrtc raa

23

<210> 21

<211> 28

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 21

ttcacagtgc tggacatcgc aggagata

28

<210> 22

<211> 28

<212> DNA

<213> Artificial

3 9 / 4 9

<220>

<223> an artificially synthesized primer sequence

<400> 22

tatctcctgc gatgtccagc actgtgaa

28

<210> 23

<211> 26

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 23

cgaacagact tcttcaccg tgctcg

26

<210> 24

<211> 26

<212> DNA

<213> Artificial

<220>

4 0 / 4 9

<223> an artificially synthesized primer sequence

<400> 24

cgagcacggt gaaagaagtc tgttcg

26

<210> 25

<211> 30

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 25

aaacatatga ataacgccgt tttgtacgaa

30

<210> 26

<211> 30

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

4 1 / 4 9

<400> 26

aactcgagct tgcatacggt tttgttattg 30

<210> 27

<211> 30

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 27

aaacatatacgataacgcggc ttgttatgaa 30

<210> 28

<211> 30

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 28

aactcgaggc ccaaaaactaa acctgaagag 30

4 2 / 4 9

<210> 29

<211> 8

<212> PRT

<213> Artificial

<220>

<223> consensus sequence

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> "Xaa"=Asp or Glu

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> "Xaa"=hydrophobic amino acid

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> "Xaa"=low molecular weight neutral amino acid

<220>

4 3 / 4 9

<221> MISC_FEATURE

<222> (7)..(7)

<223> "Xaa"=low molecular weight neutral amino acid

<400> 29

Leu Xaa Xaa Gly Xaa Gly Xaa Gly

1 5

<210> 30

<211> 18

<212> PRT

<213> Artificial

<220>

<223> consensus sequence

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> "Xaa"=any amino acid

<220>

<221> MISC_FEATURE

<222> (8)..(8)

<223> "Xaa"=Gln or Glu

4 4 / 4 9

<220>

<221> MISC_FEATURE

<222> (9)..(9)

<223> "Xaa"=His, Lys or Gln

<220>

<221> MISC_FEATURE

<222> (13)..(13)

<223> "Xaa"=hydrophobic amino acid

<400> 30

Met Asn Asn Ala Xaa Leu Tyr Xaa Xaa Ala Asn Ser Xaa Gln Lys Arg

1

5

10

15

Asp Ala

<210> 31

<211> 9

<212> PRT

<213> Artificial

<220>

<223> consensus sequence

4 5 / 4 9

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> "Xaa"=Leu, Val or Ile

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> "Xaa"=Leu, Val or Ile

<400> 31

Xaa Leu Asp Xaa Gly Cys Gly Asp Gly

1

5

<210> 32

<211> 12

<212> PRT

<213> Artificial

<220>

<223> consensus sequence

<220>

<221> MISC_FEATURE

4 6 / 4 9

<222> (1)..(1)

<223> "Xaa"=Gln, Arg or Lys

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> "Xaa"=Leu or Val

<220>

<221> MISC_FEATURE

<222> (10)..(10)

<223> "Xaa"=Gln or Lys

<400> 32

Xaa Leu Xaa Gly Cys Asp Ile Ser Glu Xaa Met Val

1

5

10

<210> 33

<211> 13

<212> PRT

<213> Artificial

<220>

<223> consensus sequence

4 7 / 4 9

<220>

<221> MISC_FEATURE

<222> (9)..(9)

<223> "Xaa"=Cys, Thr or Ala

<400> 33

Phe Asp His Val Phe Ser Phe Tyr Xaa Leu His Trp Val

1

5

10

<210> 34

<211> 9

<212> PRT

<213> Artificial

<220>

<223> consensus sequence

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> "Xaa"=Val or Ile

<220>

<221> MISC_FEATURE

<222> (5)..(5)

4 8 / 4 9

<223> "Xaa"=Val, Ile or Leu

<220>

<221> MISC_FEATURE

<222> (8)..(8)

<223> "Xaa"=Ile or Val

<400> 34

Pro Xaa Phe Asp Xaa Tyr Arg Xaa Leu

1

5

<210> 35

<211> 12

<212> PRT

<213> Artificial

<220>

<223> consensus sequence

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> "Xaa"=Lys or Arg

<400> 35

4 9 / 4 9

Asp Val Glu Xaa Tyr Ile Ser Pro Tyr His Asp Ser

1 5 10

<210> 36

<211> 10

<212> PRT

<213> Artificial

<220>

<223> consensus sequence

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> "Xaa"=Ile, Val or Leu

<400> 36

Tyr Lys Leu Xaa Val Val Tyr Ala Arg Lys

1 5 10